

## SEQUENCE LISTING

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<110> THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS  
 REPRESENTED BY THE SECRETARY OF THE DEPARTMENT OF HEALTH AND  
 HUMAN SERVICES, CENTERS FOR DISEASE CONTROL AND PREVENTION  
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 Owen, Sherry M.

<120> IMMUNOGENIC HIV-1 MULTI-CLADE, MULTIVALENT CONSTRUCTS AND METHODS  
 OF THEIR USE

<130> 6395-67675-06

<150> PCT/US2004/009767  
 <151> 2004-03-24

<150> US 60/458,880  
 <151> 2003-03-28

<160> 64

<170> PatentIn version 3.2

<210> 1  
 <211> 1557  
 <212> DNA  
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<220>  
 <223> Construct encoding polyepitope polypeptide.

<220>  
 <221> CDS  
 <222> (12)..(1547)  
 <223> Sequence encoding MCMVCTL-ubiquitin polyepitope polypeptide.

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 1 5 10

acc ctt gag gtg gag ccc agt gac acc atc gaa aat gtg aag gcc aag 98  
 Thr Leu Glu Val Glu Pro Ser Asp Thr Ile Glu Asn Val Lys Ala Lys  
 15 20 25

atc cag gat aag gaa ggc att ccc ccc gac cag cag agg ctc atc ttt 146  
 Ile Gln Asp Lys Glu Gly Ile Pro Pro Asp Gln Gln Arg Leu Ile Phe  
 30 35 40 45

gca ggc aag cag ctg gaa gat ggc cgt act ctt tct gac tac aac atc 194  
 Ala Gly Lys Gln Leu Glu Asp Gly Arg Thr Leu Ser Asp Tyr Asn Ile  
 50 55 60

cag aag gag tcg acc ctg cac ctg gtc ctg cgt ctg aga ggt gct gag 242  
 Gln Lys Glu Ser Thr Leu His Leu Val Leu Arg Leu Arg Gly Ala Glu  
 65 70 75

ctc cgc tcc ctc tac aac acc gtg gcc acc ctc tac tgc gtg cac cag Leu Arg Ser Leu Tyr Asn Thr Val Ala Thr Leu Tyr Cys Val His Gln 80 85 90	290
cgc atc aag atc cgc ctg cgc ccc gcc gcc aag aag aag tac tgg gcc Arg Ile Lys Ile Arg Leu Arg Pro Gly Gly Lys Lys Lys Tyr Trp Ala 95 100 105	338
agc cgc gag ctg gag cgc ttc aag gcc gcc atc agc ccc cgc acc ctg Ser Arg Glu Leu Glu Arg Phe Lys Ala Ala Ile Ser Pro Arg Thr Leu 110 115 120 125	386
aac gcc tgg gtg aag gtg gtg aag gcc ttc agc ccc gag gtg atc ccc Asn Ala Trp Val Lys Val Val Lys Ala Phe Ser Pro Glu Val Ile Pro 130 135 140	434
atg ttc agc gcc ctg agc gag gcc gcc acc ccc cag gac ctg aac acc Met Phe Ser Ala Leu Ser Glu Gly Ala Thr Pro Gln Asp Leu Asn Thr 145 150 155	482
atg acc agc acc ctg cag gag cag atc gcc tgg aag gcc gcc aac ccc Met Thr Ser Thr Leu Gln Glu Gln Ile Gly Trp Lys Ala Ala Asn Pro 160 165 170	530
ccc atc ccc gtg gcc gac atc tac aag cgc tgg atc atc ctg gcc ctg Pro Ile Pro Val Gly Asp Ile Tyr Lys Arg Trp Ile Ile Leu Gly Leu 175 180 185	578
aac aag atc gtg cgc atg tac agc ccc acc agc atc ttc cgc gac tac Asn Lys Ile Val Arg Met Tyr Ser Pro Thr Ser Ile Phe Arg Asp Tyr 190 195 200 205	626
gtg gac cgc ttc tac aag acc ctg cgc gcc gtg cag aac gcc aac ccc Val Asp Arg Phe Tyr Lys Thr Leu Arg Ala Val Gln Asn Ala Asn Pro 210 215 220	674
gac tgc aag acc atc ctg aag gcc ctg gcc tgc cag gcc gtg gcc gcc Asp Cys Lys Thr Ile Leu Lys Ala Leu Ala Cys Gln Gly Val Gly Gly 225 230 235	722
ccc gcc cac aag aag gcc gcc atc acc ctg tgg cag cgc ccc ctg gtg Pro Gly His Lys Lys Ala Ala Ile Thr Leu Trp Gln Arg Pro Leu Val 240 245 250	770
acc gtg ctg gac gtg gcc gac gcc tac ttc agc gtg tgg aag gcc agc Thr Val Leu Asp Val Gly Asp Ala Tyr Phe Ser Val Trp Lys Gly Ser 255 260 265	818
ccc gcc atc ttc cag agc aag ctt cgc gcc ccc gcc cgc gcc ttc gtg Pro Ala Ile Phe Gln Ser Lys Leu Arg Gly Pro Gly Arg Ala Phe Val 270 275 280 285	866
acc atc aag gcc gcc gcc tgc acc ccc tac gac atc aac cag atg ctg Thr Ile Lys Ala Ala Ala Cys Thr Pro Tyr Asp Ile Asn Gln Met Leu 290 295 300	914

ggt acc agc atg acc aag atc ctg aag gag ccc gtg cac ggc gtg aag Gly Thr Ser Met Thr Lys Ile Leu Lys Glu Pro Val His Gly Val Lys 305 310 315	962
gcc gcc cag atc tac cag gag ccc ttc aag aac ctg aag acc ggc gag Ala Ala Gln Ile Tyr Gln Glu Pro Phe Lys Asn Leu Lys Thr Gly Glu 320 325 330	1010
ccc atc gtg ggc gcc gag acc ttc tac gtg gac ggc gcc gcc aac gtg Pro Ile Val Gly Ala Glu Thr Phe Tyr Val Asp Gly Ala Ala Asn Val 335 340 345	1058
atc tac cag tac atg gac gac ctg ctg ctg tgg aag ggc gag ggc gcc Ile Tyr Gln Tyr Met Asp Asp Leu Leu Leu Trp Lys Gly Glu Gly Ala 350 355 360 365	1106
gtg aag gcc gcc cgc atc cgc acc tgg aag agc ctg gtg aag cac ccc Val Lys Ala Ala Arg Ile Arg Thr Trp Lys Ser Leu Val Lys His Pro 370 375 380	1154
aag gtg agc agc gag gtg cac atc gcc gtg cgc cac ttc ccc cgc atc Lys Val Ser Ser Glu Val His Ile Ala Val Arg His Phe Pro Arg Ile 385 390 395	1202
tgg gcc gtg cgc cac ttc ccc cgc ccc tgg gcc atc atc cgc atc ctg Trp Ala Val Arg His Phe Pro Arg Pro Trp Ala Ile Ile Arg Ile Leu 400 405 410	1250
cag cag ctg aag gcc gcc gtg ggc ttc ccc gtg cgc ccc cag gtg ccc Gln Gln Leu Lys Ala Ala Val Gly Phe Pro Val Arg Pro Gln Val Pro 415 420 425	1298
ctg cgc ccc atg acc tac aag ggc gcc gtg gac ctg agc cac ttc ctg Leu Arg Pro Met Thr Tyr Lys Gly Ala Val Asp Leu Ser His Phe Leu 430 435 440 445	1346
aag gag aag ggc ggc ctg ggc ccc ggc gtg cgc tac ccc ctg acc ttc Lys Glu Lys Gly Gly Leu Gly Pro Gly Val Arg Tyr Pro Leu Thr Phe 450 455 460	1394
ggc tgg tgc tac aag gcc gcc aag acc ctg ccc ctg tgc gtg acc ctg Gly Trp Cys Tyr Lys Ala Ala Lys Thr Leu Pro Leu Cys Val Thr Leu 465 470 475	1442
acc gtg tac tac ggc gtg ccc gtg tgg aag gag gcc acc acc acc ctg Thr Val Tyr Tyr Gly Val Pro Val Trp Lys Glu Ala Thr Thr Thr Leu 480 485 490	1490
cgc gcc atc gag gcc cag cag cac ctg gag cgc tac ctg aag gac ggc Arg Ala Ile Glu Ala Gln Gln His Leu Glu Arg Tyr Leu Lys Asp Gly 495 500 505	1538
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 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Construct encoding polyepitope polypeptide.

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Met Gln Ile Phe Val Lys Thr Leu Thr Gly Lys Thr Ile Thr Leu Glu  
 1 5 10 15

Val Glu Pro Ser Asp Thr Ile Glu Asn Val Lys Ala Lys Ile Gln Asp  
 20 25 30

Lys Glu Gly Ile Pro Pro Asp Gln Gln Arg Leu Ile Phe Ala Gly Lys  
 35 40 45

Gln Leu Glu Asp Gly Arg Thr Leu Ser Asp Tyr Asn Ile Gln Lys Glu  
 50 55 60

Ser Thr Leu His Leu Val Leu Arg Leu Arg Gly Ala Glu Leu Arg Ser  
 65 70 75 80

Leu Tyr Asn Thr Val Ala Thr Leu Tyr Cys Val His Gln Arg Ile Lys  
 85 90 95

Ile Arg Leu Arg Pro Gly Gly Lys Lys Lys Tyr Trp Ala Ser Arg Glu  
 100 105 110

Leu Glu Arg Phe Lys Ala Ala Ile Ser Pro Arg Thr Leu Asn Ala Trp  
 115 120 125

Val Lys Val Val Lys Ala Phe Ser Pro Glu Val Ile Pro Met Phe Ser  
 130 135 140

Ala Leu Ser Glu Gly Ala Thr Pro Gln Asp Leu Asn Thr Met Thr Ser  
 145 150 155 160

Thr Leu Gln Glu Gln Ile Gly Trp Lys Ala Ala Asn Pro Pro Ile Pro  
 165 170 175

Val Gly Asp Ile Tyr Lys Arg Trp Ile Ile Leu Gly Leu Asn Lys Ile  
 180 185 190

Val Arg Met Tyr Ser Pro Thr Ser Ile Phe Arg Asp Tyr Val Asp Arg  
195 200 205

Phe Tyr Lys Thr Leu Arg Ala Val Gln Asn Ala Asn Pro Asp Cys Lys  
210 215 220

Thr Ile Leu Lys Ala Leu Ala Cys Gln Gly Val Gly Gly Pro Gly His  
225 230 235 240

Lys Lys Ala Ala Ile Thr Leu Trp Gln Arg Pro Leu Val Thr Val Leu  
245 250 255

Asp Val Gly Asp Ala Tyr Phe Ser Val Trp Lys Gly Ser Pro Ala Ile  
260 265 270

Phe Gln Ser Lys Leu Arg Gly Pro Gly Arg Ala Phe Val Thr Ile Lys  
275 280 285

Ala Ala Ala Cys Thr Pro Tyr Asp Ile Asn Gln Met Leu Gly Thr Ser  
290 295 300

Met Thr Lys Ile Leu Lys Glu Pro Val His Gly Val Lys Ala Ala Gln  
305 310 315 320

Ile Tyr Gln Glu Pro Phe Lys Asn Leu Lys Thr Gly Glu Pro Ile Val  
325 330 335

Gly Ala Glu Thr Phe Tyr Val Asp Gly Ala Ala Asn Val Ile Tyr Gln  
340 345 350

Tyr Met Asp Asp Leu Leu Leu Trp Lys Gly Glu Gly Ala Val Lys Ala  
355 360 365

Ala Arg Ile Arg Thr Trp Lys Ser Leu Val Lys His Pro Lys Val Ser  
370 375 380

Ser Glu Val His Ile Ala Val Arg His Phe Pro Arg Ile Trp Ala Val  
385 390 395 400

Arg His Phe Pro Arg Pro Trp Ala Ile Ile Arg Ile Leu Gln Gln Leu  
405 410 415

Lys Ala Ala Val Gly Phe Pro Val Arg Pro Gln Val Pro Leu Arg Pro  
420 425 430

Met Thr Tyr Lys Gly Ala Val Asp Leu Ser His Phe Leu Lys Glu Lys  
435 440 445

Gly Gly Leu Gly Pro Gly Val Arg Tyr Pro Leu Thr Phe Gly Trp Cys  
450 455 460

Tyr Lys Ala Ala Lys Thr Leu Pro Leu Cys Val Thr Leu Thr Val Tyr  
465 470 475 480

Tyr Gly Val Pro Val Trp Lys Glu Ala Thr Thr Thr Leu Arg Ala Ile  
485 490 495

Glu Ala Gln Gln His Leu Glu Arg Tyr Leu Lys Asp Gly Gly Leu  
500 505 510

<210> 3  
<211> 1323  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Construct encoding polyepitope polypeptide.

<220>  
<221> CDS  
<222> (7)..(1317)  
<223> Sequence encoding MCMVCTL (no ubiquitin) polyepitope polypeptide.

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tgc gtg cac cag cgc atc aag atc cgc ctg cgc ccc gcc gcc aag aag 96  
Cys Val His Gln Arg Ile Lys Ile Arg Leu Arg Pro Gly Gly Lys Lys  
15 20 25 30

aag tac tgg gcc agc cgc gag ctg gag cgc ttc aag gcc gcc atc agc 144  
Lys Tyr Trp Ala Ser Arg Glu Leu Glu Arg Phe Lys Ala Ala Ile Ser  
35 40 45

ccc cgc acc ctg aac gcc tgg gtg aag gtg gtg aag gcc ttc agc ccc 192  
Pro Arg Thr Leu Asn Ala Trp Val Lys Val Val Lys Ala Phe Ser Pro  
50 55 60

gag gtg atc ccc atg ttc agc gcc ctg agc gag gcc gcc acc ccc cag 240  
Glu Val Ile Pro Met Phe Ser Ala Leu Ser Glu Gly Ala Thr Pro Gln

65					70					75						
gac	ctg	aac	acc	atg	acc	agc	acc	ctg	cag	gag	cag	atc	ggc	tgg	aag	288
Asp	Leu	Asn	Thr	Met	Thr	Ser	Thr	Leu	Gln	Glu	Gln	Ile	Gly	Trp	Lys	
80						85					90					
gcc	gcc	aac	ccc	ccc	atc	ccc	gtg	ggc	gac	atc	tac	aag	cgc	tgg	atc	336
Ala	Ala	Asn	Pro	Pro	Ile	Pro	Val	Gly	Asp	Ile	Tyr	Lys	Arg	Trp	Ile	
95					100					105					110	
atc	ctg	ggc	ctg	aac	aag	atc	gtg	cgc	atg	tac	agc	ccc	acc	agc	atc	384
Ile	Leu	Gly	Leu	Asn	Lys	Ile	Val	Arg	Met	Tyr	Ser	Pro	Thr	Ser	Ile	
				115					120					125		
ttc	cgc	gac	tac	gtg	gac	cgc	ttc	tac	aag	acc	ctg	cgc	gcc	gtg	cag	432
Phe	Arg	Asp	Tyr	Val	Asp	Arg	Phe	Tyr	Lys	Thr	Leu	Arg	Ala	Val	Gln	
			130					135					140			
aac	gcc	aac	ccc	gac	tgc	aag	acc	atc	ctg	aag	gcc	ctg	gcc	tgc	cag	480
Asn	Ala	Asn	Pro	Asp	Cys	Lys	Thr	Ile	Leu	Lys	Ala	Leu	Ala	Cys	Gln	
		145					150					155				
ggc	gtg	ggc	ggc	ccc	ggc	cac	aag	aag	gcc	gcc	atc	acc	ctg	tgg	cag	528
Gly	Val	Gly	Gly	Pro	Gly	His	Lys	Lys	Ala	Ala	Ile	Thr	Leu	Trp	Gln	
	160					165					170					
cgc	ccc	ctg	gtg	acc	gtg	ctg	gac	gtg	ggc	gac	gcc	tac	ttc	agc	gtg	576
Arg	Pro	Leu	Val	Thr	Val	Leu	Asp	Val	Gly	Asp	Ala	Tyr	Phe	Ser	Val	
175					180					185					190	
tgg	aag	ggc	agc	ccc	gcc	atc	ttc	cag	agc	aag	ctt	cgc	ggc	ccc	ggc	624
Trp	Lys	Gly	Ser	Pro	Ala	Ile	Phe	Gln	Ser	Lys	Leu	Arg	Gly	Pro	Gly	
				195					200					205		
cgc	gcc	ttc	gtg	acc	atc	aag	gcc	gcc	gcc	tgc	acc	ccc	tac	gac	atc	672
Arg	Ala	Phe	Val	Thr	Ile	Lys	Ala	Ala	Ala	Cys	Thr	Pro	Tyr	Asp	Ile	
			210					215					220			
aac	cag	atg	ctg	ggc	acc	agc	atg	acc	aag	atc	ctg	aag	gag	ccc	gtg	720
Asn	Gln	Met	Leu	Gly	Thr	Ser	Met	Thr	Lys	Ile	Leu	Lys	Glu	Pro	Val	
		225					230					235				
cac	ggc	gtg	aag	gcc	gcc	cag	atc	tac	cag	gag	ccc	ttc	aag	aac	ctg	768
His	Gly	Val	Lys	Ala	Ala	Gln	Ile	Tyr	Gln	Glu	Pro	Phe	Lys	Asn	Leu	
		240				245					250					
aag	acc	ggc	gag	ccc	atc	gtg	ggc	gcc	gag	acc	ttc	tac	gtg	gac	ggc	816
Lys	Thr	Gly	Glu	Pro	Ile	Val	Gly	Ala	Glu	Thr	Phe	Tyr	Val	Asp	Gly	
255					260					265					270	
gcc	gcc	aac	gtg	atc	tac	cag	tac	atg	gac	gac	ctg	ctg	ctg	tgg	aag	864
Ala	Ala	Asn	Val	Ile	Tyr	Gln	Tyr	Met	Asp	Asp	Leu	Leu	Leu	Trp	Lys	
				275					280					285		
ggc	gag	ggc	gcc	gtg	aag	gcc	gcc	cgc	atc	cgc	acc	tgg	aag	agc	ctg	912
Gly	Glu	Gly	Ala	Val	Lys	Ala	Ala	Arg	Ile	Arg	Thr	Trp	Lys	Ser	Leu	
			290					295					300			

gtg aag cac ccc aag gtg agc agc gag gtg cac atc gcc gtg cgc cac	960
Val Lys His Pro Lys Val Ser Ser Glu Val His Ile Ala Val Arg His	
305 310 315	
ttc ccc cgc atc tgg gcc gtg cgc cac ttc ccc cgc ccc tgg gcc atc	1008
Phe Pro Arg Ile Trp Ala Val Arg His Phe Pro Arg Pro Trp Ala Ile	
320 325 330	
atc cgc atc ctg cag cag ctg aag gcc gcc gtg ggc ttc ccc gtg cgc	1056
Ile Arg Ile Leu Gln Gln Leu Lys Ala Ala Val Gly Phe Pro Val Arg	
335 340 345 350	
ccc cag gtg ccc ctg cgc ccc atg acc tac aag ggc gcc gtg gac ctg	1104
Pro Gln Val Pro Leu Arg Pro Met Thr Tyr Lys Gly Ala Val Asp Leu	
355 360 365	
agc cac ttc ctg aag gag aag ggc ggc ctg ggc ccc ggc gtg cgc tac	1152
Ser His Phe Leu Lys Glu Lys Gly Gly Leu Gly Pro Gly Val Arg Tyr	
370 375 380	
ccc ctg acc ttc ggc tgg tgc tac aag gcc gcc aag acc ctg ccc ctg	1200
Pro Leu Thr Phe Gly Trp Cys Tyr Lys Ala Ala Lys Thr Leu Pro Leu	
385 390 395	
tgc gtg acc ctg acc gtg tac tac ggc gtg ccc gtg tgg aag gag gcc	1248
Cys Val Thr Leu Thr Val Tyr Tyr Gly Val Pro Val Trp Lys Glu Ala	
400 405 410	
acc acc acc ctg cgc gcc atc gag gcc cag cag cac ctg gag cgc tac	1296
Thr Thr Thr Leu Arg Ala Ile Glu Ala Gln Gln His Leu Glu Arg Tyr	
415 420 425 430	
ctg aag gac ggc ggc ctg tag ctcgag	1323
Leu Lys Asp Gly Gly Leu	
435	

<210> 4  
 <211> 436  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Construct encoding polyepitope polypeptide.

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Met Glu Leu Arg Ser Leu Tyr Asn Thr Val Ala Thr Leu Tyr Cys Val	
1 5 10 15	
His Gln Arg Ile Lys Ile Arg Leu Arg Pro Gly Gly Lys Lys Lys Tyr	
20 25 30	
Trp Ala Ser Arg Glu Leu Glu Arg Phe Lys Ala Ala Ile Ser Pro Arg	

35	40	45
Thr Leu Asn Ala Trp Val Lys Val Val Lys Ala Phe Ser Pro Glu Val		
50	55	60
Ile Pro Met Phe Ser Ala Leu Ser Glu Gly Ala Thr Pro Gln Asp Leu		
65	70	75
Asn Thr Met Thr Ser Thr Leu Gln Glu Gln Ile Gly Trp Lys Ala Ala		
	85	90
		95
Asn Pro Pro Ile Pro Val Gly Asp Ile Tyr Lys Arg Trp Ile Ile Leu		
	100	105
		110
Gly Leu Asn Lys Ile Val Arg Met Tyr Ser Pro Thr Ser Ile Phe Arg		
	115	120
		125
Asp Tyr Val Asp Arg Phe Tyr Lys Thr Leu Arg Ala Val Gln Asn Ala		
	130	135
		140
Asn Pro Asp Cys Lys Thr Ile Leu Lys Ala Leu Ala Cys Gln Gly Val		
145	150	155
		160
Gly Gly Pro Gly His Lys Lys Ala Ala Ile Thr Leu Trp Gln Arg Pro		
	165	170
		175
Leu Val Thr Val Leu Asp Val Gly Asp Ala Tyr Phe Ser Val Trp Lys		
	180	185
		190
Gly Ser Pro Ala Ile Phe Gln Ser Lys Leu Arg Gly Pro Gly Arg Ala		
	195	200
		205
Phe Val Thr Ile Lys Ala Ala Ala Cys Thr Pro Tyr Asp Ile Asn Gln		
	210	215
		220
Met Leu Gly Thr Ser Met Thr Lys Ile Leu Lys Glu Pro Val His Gly		
225	230	235
		240
Val Lys Ala Ala Gln Ile Tyr Gln Glu Pro Phe Lys Asn Leu Lys Thr		
	245	250
		255
Gly Glu Pro Ile Val Gly Ala Glu Thr Phe Tyr Val Asp Gly Ala Ala		
	260	265
		270

Asn Val Ile Tyr Gln Tyr Met Asp Asp Leu Leu Leu Trp Lys Gly Glu  
275 280 285

Gly Ala Val Lys Ala Ala Arg Ile Arg Thr Trp Lys Ser Leu Val Lys  
290 295 300

His Pro Lys Val Ser Ser Glu Val His Ile Ala Val Arg His Phe Pro  
305 310 315 320

Arg Ile Trp Ala Val Arg His Phe Pro Arg Pro Trp Ala Ile Ile Arg  
325 330 335

Ile Leu Gln Gln Leu Lys Ala Ala Val Gly Phe Pro Val Arg Pro Gln  
340 345 350

Val Pro Leu Arg Pro Met Thr Tyr Lys Gly Ala Val Asp Leu Ser His  
355 360 365

Phe Leu Lys Glu Lys Gly Gly Leu Gly Pro Gly Val Arg Tyr Pro Leu  
370 375 380

Thr Phe Gly Trp Cys Tyr Lys Ala Ala Lys Thr Leu Pro Leu Cys Val  
385 390 395 400

Thr Leu Thr Val Tyr Tyr Gly Val Pro Val Trp Lys Glu Ala Thr Thr  
405 410 415

Thr Leu Arg Ala Ile Glu Ala Gln Gln His Leu Glu Arg Tyr Leu Lys  
420 425 430

Asp Gly Gly Leu  
435

<210> 5  
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<213> Artificial Sequence

<220>  
<223> Polyepitope polypeptide.

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Lys Glu Gly Ile Pro Pro Asp Gln Gln Arg Leu Ile Phe Ala Gly Lys	35	40	45
Gln Leu Glu Asp Gly Arg Thr Leu Ser Asp Tyr Asn Ile Gln Lys Glu	50	55	60
Ser Thr Leu His Leu Val Leu Arg Leu Arg Gly Ala Glu Leu Arg Ser	65	70	75
Leu Tyr Asn Thr Val Ala Thr Leu Tyr Cys Val His Gln Arg Ile Lys	85	90	95
Ile Arg Leu Arg Pro Gly Gly Lys Lys Lys Tyr Trp Ala Ser Arg Glu	100	105	110
Leu Glu Arg Phe Lys Ala Ala Ile Ser Pro Arg Thr Leu Asn Ala Trp	115	120	125
Val Lys Val Val Lys Ala Phe Ser Pro Glu Val Ile Pro Met Phe Ser	130	135	140
Ala Leu Ser Glu Gly Ala Thr Pro Gln Asp Leu Asn Thr Met Thr Ser	145	150	155
Thr Leu Gln Glu Gln Ile Gly Trp Lys Ala Ala Asn Pro Pro Ile Pro	165	170	175
Val Gly Asp Ile Tyr Lys Arg Trp Ile Ile Leu Gly Leu Asn Lys Ile	180	185	190
Val Arg Met Tyr Ser Pro Thr Ser Ile Phe Arg Asp Tyr Val Asp Arg	195	200	205
Phe Tyr Lys Thr Leu Arg Ala Val Gln Asn Ala Asn Pro Asp Cys Lys	210	215	220
Thr Ile Leu Lys Ala Leu Ala Cys Gln Gly Val Gly Gly Pro Gly His	225	230	235
			240

Lys Lys Ala Ala Ile Thr Leu Trp Gln Arg Pro Leu Val Thr Val Leu  
245 250 255

Asp Val Gly Asp Ala Tyr Phe Ser Val Trp Lys Gly Ser Pro Ala Ile  
260 265 270

Phe Gln Ser Lys Leu Gly Thr Ser Met Thr Lys Ile Leu Lys Glu Pro  
275 280 285

Val His Gly Val Lys Ala Ala Gln Ile Tyr Gln Glu Pro Phe Lys Asn  
290 295 300

Leu Lys Thr Gly Glu Pro Ile Val Gly Ala Glu Thr Phe Tyr Val Asp  
305 310 315 320

Gly Ala Ala Asn Val Ile Tyr Gln Tyr Met Asp Asp Leu Leu Leu Trp  
325 330 335

Lys Gly Glu Gly Ala Val Lys Ala Ala Arg Ile Arg Thr Trp Lys Ser  
340 345 350

Leu Val Lys His Pro Lys Val Ser Ser Glu Val His Ile Ala Val Arg  
355 360 365

His Phe Pro Arg Ile Trp Ala Val Arg His Phe Pro Arg Pro Trp Ala  
370 375 380

Ile Ile Arg Ile Leu Gln Gln Leu Lys Ala Ala Val Gly Phe Pro Val  
385 390 395 400

Arg Pro Gln Val Pro Leu Arg Pro Met Thr Tyr Lys Gly Ala Val Asp  
405 410 415

Leu Ser His Phe Leu Lys Glu Lys Gly Gly Leu Gly Pro Gly Val Arg  
420 425 430

Tyr Pro Leu Thr Phe Gly Trp Cys Tyr Lys Ala Ala Lys Thr Leu Pro  
435 440 445

Leu Cys Val Thr Leu Thr Val Tyr Tyr Gly Val Pro Val Trp Lys Glu  
450 455 460

Ala Thr Thr Thr Leu Arg Ala Ile Glu Ala Gln Gln His Leu Glu Arg  
 465 470 475 480

Tyr Leu Lys Asp Gly Gly Leu  
 485

<210> 6

<211> 412

<212> PRT

<213> Artificial Sequence

<220>

<223> Polyepitope polypeptide.

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Met Glu Leu Arg Ser Leu Tyr Asn Thr Val Ala Thr Leu Tyr Cys Val  
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His Gln Arg Ile Lys Ile Arg Leu Arg Pro Gly Gly Lys Lys Lys Tyr  
 20 25 30

Trp Ala Ser Arg Glu Leu Glu Arg Phe Lys Ala Ala Ile Ser Pro Arg  
 35 40 45

Thr Leu Asn Ala Trp Val Lys Val Val Lys Ala Phe Ser Pro Glu Val  
 50 55 60

Ile Pro Met Phe Ser Ala Leu Ser Glu Gly Ala Thr Pro Gln Asp Leu  
 65 70 75 80

Asn Thr Met Thr Ser Thr Leu Gln Glu Gln Ile Gly Trp Lys Ala Ala  
 85 90 95

Asn Pro Pro Ile Pro Val Gly Asp Ile Tyr Lys Arg Trp Ile Ile Leu  
 100 105 110

Gly Leu Asn Lys Ile Val Arg Met Tyr Ser Pro Thr Ser Ile Phe Arg  
 115 120 125

Asp Tyr Val Asp Arg Phe Tyr Lys Thr Leu Arg Ala Val Gln Asn Ala  
 130 135 140

Asn Pro Asp Cys Lys Thr Ile Leu Lys Ala Leu Ala Cys Gln Gly Val  
 145 150 155 160

Gly Gly Pro Gly His Lys Lys Ala Ala Ile Thr Leu Trp Gln Arg Pro  
165 170 175

Leu Val Thr Val Leu Asp Val Gly Asp Ala Tyr Phe Ser Val Trp Lys  
180 185 190

Gly Ser Pro Ala Ile Phe Gln Ser Lys Leu Gly Thr Ser Met Thr Lys  
195 200 205

Ile Leu Lys Glu Pro Val His Gly Val Lys Ala Ala Gln Ile Tyr Gln  
210 215 220

Glu Pro Phe Lys Asn Leu Lys Thr Gly Glu Pro Ile Val Gly Ala Glu  
225 230 235 240

Thr Phe Tyr Val Asp Gly Ala Ala Asn Val Ile Tyr Gln Tyr Met Asp  
245 250 255

Asp Leu Leu Leu Trp Lys Gly Glu Gly Ala Val Lys Ala Ala Arg Ile  
260 265 270

Arg Thr Trp Lys Ser Leu Val Lys His Pro Lys Val Ser Ser Glu Val  
275 280 285

His Ile Ala Val Arg His Phe Pro Arg Ile Trp Ala Val Arg His Phe  
290 295 300

Pro Arg Pro Trp Ala Ile Ile Arg Ile Leu Gln Gln Leu Lys Ala Ala  
305 310 315 320

Val Gly Phe Pro Val Arg Pro Gln Val Pro Leu Arg Pro Met Thr Tyr  
325 330 335

Lys Gly Ala Val Asp Leu Ser His Phe Leu Lys Glu Lys Gly Gly Leu  
340 345 350

Gly Pro Gly Val Arg Tyr Pro Leu Thr Phe Gly Trp Cys Tyr Lys Ala  
355 360 365

Ala Lys Thr Leu Pro Leu Cys Val Thr Leu Thr Val Tyr Tyr Gly Val  
370 375 380

Pro Val Trp Lys Glu Ala Thr Thr Thr Leu Arg Ala Ile Glu Ala Gln  
 385 390 395 400

Gln His Leu Glu Arg Tyr Leu Lys Asp Gly Gly Leu  
 405 410

<210> 7  
 <211> 2126  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Construct encoding polyepitope polypeptide.

<220>  
 <221> CDS  
 <222> (7)..(2118)  
 <223> Sequence encoding MCMVABTh-LIMPPII polyepitope polypeptide.

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 Met Ala Cys Thr Asn Cys Tyr Cys Lys Lys Cys Cys Phe His  
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tgc cag gtg tgc ttc acc acc ggc ccc ggc ccc cgc cag cgc cgc cgc 96  
 Cys Gln Val Cys Phe Thr Thr Gly Pro Gly Pro Arg Gln Arg Arg Arg  
 15 20 25 30

gcc ccc cag gac agc cag acc cac cag gtg agc gta tac tac gcc gcc 144  
 Ala Pro Gln Asp Ser Gln Thr His Gln Val Ser Val Tyr Tyr Ala Ala  
 35 40 45

gcc cag tgg gac ttc ggc aac acc atg tgc cag atc aat ccc ggc cgc 192  
 Ala Gln Trp Asp Phe Gly Asn Thr Met Cys Gln Ile Asn Pro Gly Arg  
 50 55 60

agc cag aag gag ggc ctg cac tac acc tgc gta tac ggc ccc ggc ccc 240  
 Ser Gln Lys Glu Gly Leu His Tyr Thr Cys Val Tyr Gly Pro Gly Pro  
 65 70 75

ccc tgc aac aag tgc tac tgc aag aag tgc tgc tac cac tgc cag gtg 288  
 Pro Cys Asn Lys Cys Tyr Cys Lys Lys Cys Cys Tyr His Cys Gln Val  
 80 85 90

tgc ttc ctg aac aat ccc ggc aag cag cgc cgc ggc acc ccc cag agc 336  
 Cys Phe Leu Asn Asn Pro Gly Lys Gln Arg Arg Gly Thr Pro Gln Ser  
 95 100 105 110

aac aag gac cac cag aac ccc ggc cct gga ccc aac gag cag gac ctg 384  
 Asn Lys Asp His Gln Asn Pro Gly Pro Gly Pro Asn Glu Gln Asp Leu  
 115 120 125

ctg gcc ctg gac aag tgg gcc aac ctg tgg aac tgg ttc gac atc agc 432

Leu	Ala	Leu	Asp	Lys	Trp	Ala	Asn	Leu	Trp	Asn	Trp	Phe	Asp	Ile	Ser		
			130					135					140				
aat	ccc	ggc	gcc	tgc	aac	acc	tgc	tac	tgc	aag	aag	tgc	agc	tac	cac	480	
Asn	Pro	Gly	Ala	Cys	Asn	Thr	Cys	Tyr	Cys	Lys	Lys	Cys	Ser	Tyr	His		
		145					150					155					
tgc	ctg	gtg	tgc	ttc	cag	acc	ggc	ccc	ggc	ccc	cgc	cag	cgc	cgc	agc	528	
Cys	Leu	Val	Cys	Phe	Gln	Thr	Gly	Pro	Gly	Pro	Arg	Gln	Arg	Arg	Ser		
	160					165					170						
gcc	ccc	ccc	agc	agc	gag	gac	cac	cag	aac	ctg	aat	ccc	ggc	aac	gag	576	
Ala	Pro	Pro	Ser	Ser	Glu	Asp	His	Gln	Asn	Leu	Asn	Pro	Gly	Asn	Glu		
175					180					185					190		
cag	gag	ctg	ctg	gag	ctg	gac	aag	tgg	gcc	agc	ctg	tgg	aac	tgg	ttc	624	
Gln	Glu	Leu	Leu	Glu	Leu	Asp	Lys	Trp	Ala	Ser	Leu	Trp	Asn	Trp	Phe		
				195				200						205			
gac	atc	acc	ggc	cca	gga	ccc	cac	gag	cgc	agc	tac	atg	ttc	agc	gac	672	
Asp	Ile	Thr	Gly	Pro	Gly	Pro	His	Glu	Arg	Ser	Tyr	Met	Phe	Ser	Asp		
			210					215				220					
ctg	gag	aac	cgc	tgc	atc	aac	gag	aag	gac	ctg	ctg	gcc	ctg	gac	aag	720	
Leu	Glu	Asn	Arg	Cys	Ile	Asn	Glu	Lys	Asp	Leu	Leu	Ala	Leu	Asp	Lys		
		225				230						235					
tgg	cag	aac	ctg	tgg	agc	tgg	ttc	gac	atc	acc	aac	cct	ggc	agc	ggc	768	
Trp	Gln	Asn	Leu	Trp	Ser	Trp	Phe	Asp	Ile	Thr	Asn	Pro	Gly	Ser	Gly		
	240					245					250						
atc	gtg	cag	cag	cag	aac	aac	ctg	ctg	cgc	gcc	atc	gag	gcc	cag	cag	816	
Ile	Val	Gln	Gln	Gln	Asn	Asn	Leu	Leu	Arg	Ala	Ile	Glu	Ala	Gln	Gln		
255					260					265					270		
cac	ctg	ctg	cag	ctg	acc	acc	gtg	tgg	ggc	atc	aag	cag	ctg	cag	gcc	864	
His	Leu	Leu	Gln	Leu	Thr	Thr	Val	Trp	Gly	Ile	Lys	Gln	Leu	Gln	Ala		
				275				280						285			
cgc	atc	ctg	aat	ccc	ggc	ggt	cct	gga	cca	tgg	atg	gag	tgg	gac	cgc	912	
Arg	Ile	Leu	Asn	Pro	Gly	Gly	Pro	Gly	Pro	Trp	Met	Glu	Trp	Asp	Arg		
			290				295					300					
gag	atc	aac	aac	tac	acc	agc	ctg	atc	cac	agc	ctg	atc	gag	gag	agc	960	
Glu	Ile	Asn	Asn	Tyr	Thr	Ser	Leu	Ile	His	Ser	Leu	Ile	Glu	Glu	Ser		
		305					310					315					
cag	aac	cag	cag	gag	aag	aac	gag	cag	gag	ctg	ctg	tct	aga	ccc	ggg	1008	
Gln	Asn	Gln	Gln	Glu	Lys	Asn	Glu	Gln	Glu	Leu	Leu	Ser	Arg	Pro	Gly		
	320					325					330						
ggt	acc	atg	gcc	ttc	agc	ccc	gag	gtg	atc	ccc	atg	ttc	agc	gcc	ctg	1056	
Gly	Thr	Met	Ala	Phe	Ser	Pro	Glu	Val	Ile	Pro	Met	Phe	Ser	Ala	Leu		
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agc	gag	ggc	gcc	acc	ccc	cag	gac	ctg	ccc	atc	gtg	cag	aac	atc	cag	1104	
Ser	Glu	Gly	Ala	Thr	Pro	Gln	Asp	Leu	Pro	Ile	Val	Gln	Asn	Ile	Gln		

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ggc	cag	atg	gtg	cac	cag	gcc	atc	agc	ccc	cgc	acc	ctg	aac	gcc	ggc	1152				
Gly	Gln	Met	Val	His	Gln	Ala	Ile	Ser	Pro	Arg	Thr	Leu	Asn	Ala	Gly					
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ccc	ggc	ccc	ctg	cag	gag	cag	atc	ggc	tgg	atg	acc	aac	aac	ccc	ccc	1200				
Pro	Gly	Pro	Leu	Gln	Glu	Gln	Ile	Gly	Trp	Met	Thr	Asn	Asn	Pro	Pro					
		385					390					395								
atc	ccc	gtg	ggc	gag	atc	tac	aag	cgc	tgg	atc	atc	ctg	ggc	ctg	aac	1248				
Ile	Pro	Val	Gly	Glu	Ile	Tyr	Lys	Arg	Trp	Ile	Ile	Leu	Gly	Leu	Asn					
	400					405					410									
aag	atc	gtg	cgc	atg	tac	agc	ccc	acc	agc	atc	ctg	gac	atc	cgc	cag	1296				
Lys	Ile	Val	Arg	Met	Tyr	Ser	Pro	Thr	Ser	Ile	Leu	Asp	Ile	Arg	Gln					
415					420				425						430					
ggc	ccc	aag	gag	ccc	ttc	cgc	gac	tac	gtg	gac	cgc	ttc	tac	aag	gag	1344				
Gly	Pro	Lys	Glu	Pro	Phe	Arg	Asp	Tyr	Val	Asp	Arg	Phe	Tyr	Lys	Glu					
				435					440					445						
atc	tgc	acc	gag	atg	gag	aag	gag	ggc	aag	atc	agc	aag	atc	ggc	ccc	1392				
Ile	Cys	Thr	Glu	Met	Glu	Lys	Glu	Gly	Lys	Ile	Ser	Lys	Ile	Gly	Pro					
			450					455					460							
ggc	ccc	ggc	ccc	ttc	cgc	aag	tac	acc	gcc	ttc	acc	atc	ccc	agc	atc	1440				
Gly	Pro	Gly	Pro	Phe	Arg	Lys	Tyr	Thr	Ala	Phe	Thr	Ile	Pro	Ser	Ile					
		465					470					475								
aac	aac	gag	agc	ccc	gcc	atc	ttc	cag	agc	agc	atg	acc	aag	atc	ctg	1488				
Asn	Asn	Glu	Ser	Pro	Ala	Ile	Phe	Gln	Ser	Ser	Met	Thr	Lys	Ile	Leu					
	480					485					490									
gag	ccc	tgg	gag	ttc	gtg	aac	acc	ccc	ccc	ctg	gtg	aag	ctg	tgg	tac	1536				
Glu	Pro	Trp	Glu	Phe	Val	Asn	Thr	Pro	Pro	Leu	Val	Lys	Leu	Trp	Tyr					
495					500				505						510					
cag	aag	acc	gcc	gtg	cag	atg	gcc	gtg	ttc	atc	cac	aac	ttc	aag	cgc	1584				
Gln	Lys	Thr	Ala	Val	Gln	Met	Ala	Val	Phe	Ile	His	Asn	Phe	Lys	Arg					
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cag	aag	cag	atc	acc	aag	atc	cag	aac	ttc	cgc	gtg	tac	tac	cgc	ggc	1632				
Gln	Lys	Gln	Ile	Thr	Lys	Ile	Gln	Asn	Phe	Arg	Val	Tyr	Tyr	Arg	Gly					
			530				535					540								
ccc	ggc	ccc	cag	ctg	ctg	ttc	atc	cac	ttc	cgc	tcg	cgc	cag	cgg	cgg	1680				
Pro	Gly	Pro	Gln	Leu	Leu	Phe	Ile	His	Phe	Arg	Ser	Arg	Gln	Arg	Arg					
		545				550					555									
cgg	cgg	tac	agc	agc	ttg	atc	agg	cgc	acg	gtg	cgg	atc	agc	tcc	tcg	1728				
Arg	Arg	Tyr	Ser	Ser	Leu	Ile	Arg	Arg	Thr	Val	Arg	Ile	Ser	Ser	Ser					
	560					565				570										
tcg	cgg	ctg	tgg	cgg	cag	ccg	atg	cgg	aag	tgg	atg	aac	agc	agc	atc	1776				
Ser	Arg	Leu	Trp	Arg	Gln	Pro	Met	Arg	Lys	Trp	Met	Asn	Ser	Ser	Ile					
575				580				585							590					

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Ser Gly Pro Gly Pro Asp Met Arg Asp Asn Trp Arg Ser Glu Leu Tyr	
595 600 605	
aag tac aag gtg cag cag cac ctg ctg cag ctg acc gtg tgg ggc atc	1872
Lys Tyr Lys Val Gln Gln His Leu Leu Gln Leu Thr Val Trp Gly Ile	
610 615 620	
aag cag ctg gcc agc ctg tgg aac tgg ttc gac atc acc aac tgg ctg	1920
Lys Gln Leu Ala Ser Leu Trp Asn Trp Phe Asp Ile Thr Asn Trp Leu	
625 630 635	
tgg tac atc aag atc ttc atc atg atc gtg ggc ggc ctg atc ggc ctg	1968
Trp Tyr Ile Lys Ile Phe Ile Met Ile Val Gly Gly Leu Ile Gly Leu	
640 645 650	
cgc cac atc ccc cgc cgc atc cgc cag ggc ctg gag cgc gcc ctg agg	2016
Arg His Ile Pro Arg Arg Ile Arg Gln Gly Leu Glu Arg Ala Leu Arg	
655 660 665 670	
gca gca tgg acg agg gca ccg ccg acg agc gcg ccc ccc cgc ggc cag	2064
Ala Ala Trp Thr Arg Ala Pro Pro Thr Ser Ala Pro Pro Arg Gly Gln	
675 680 685	
ggc agc atg gac gag ggc acc gcc gac gag cgc gcc ccc ctg atc cgc	2112
Gly Ser Met Asp Glu Gly Thr Ala Asp Glu Arg Ala Pro Leu Ile Arg	
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acc tga gtttaaacc	2126
Thr	

<210> 8  
 <211> 703  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Construct encoding polyepitope polypeptide.

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Gln Asp Ser Gln Thr His Gln Val Ser Val Tyr Tyr Ala Ala Ala Gln
35 40 45

Trp Asp Phe Gly Asn Thr Met Cys Gln Ile Asn Pro Gly Arg Ser Gln
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50		55		60
Lys Glu Gly Leu His Tyr Thr Cys Val Tyr Gly Pro Gly Pro Pro Cys				
65		70		75 80
Asn Lys Cys Tyr Cys Lys Lys Cys Cys Tyr His Cys Gln Val Cys Phe				
	85		90	95
Leu Asn Asn Pro Gly Lys Gln Arg Arg Gly Thr Pro Gln Ser Asn Lys				
	100		105	110
Asp His Gln Asn Pro Gly Pro Gly Pro Asn Glu Gln Asp Leu Leu Ala				
	115		120	125
Leu Asp Lys Trp Ala Asn Leu Trp Asn Trp Phe Asp Ile Ser Asn Pro				
	130		135	140
Gly Ala Cys Asn Thr Cys Tyr Cys Lys Lys Cys Ser Tyr His Cys Leu				
145		150		155 160
Val Cys Phe Gln Thr Gly Pro Gly Pro Arg Gln Arg Arg Ser Ala Pro				
	165		170	175
Pro Ser Ser Glu Asp His Gln Asn Leu Asn Pro Gly Asn Glu Gln Glu				
	180		185	190
Leu Leu Glu Leu Asp Lys Trp Ala Ser Leu Trp Asn Trp Phe Asp Ile				
	195		200	205
Thr Gly Pro Gly Pro His Glu Arg Ser Tyr Met Phe Ser Asp Leu Glu				
	210		215	220
Asn Arg Cys Ile Asn Glu Lys Asp Leu Leu Ala Leu Asp Lys Trp Gln				
225		230		235 240
Asn Leu Trp Ser Trp Phe Asp Ile Thr Asn Pro Gly Ser Gly Ile Val				
	245		250	255
Gln Gln Gln Asn Asn Leu Leu Arg Ala Ile Glu Ala Gln Gln His Leu				
	260		265	270
Leu Gln Leu Thr Thr Val Trp Gly Ile Lys Gln Leu Gln Ala Arg Ile				
	275		280	285

Leu Asn Pro Gly Gly Pro Gly Pro Trp Met Glu Trp Asp Arg Glu Ile  
 290 295 300

Asn Asn Tyr Thr Ser Leu Ile His Ser Leu Ile Glu Glu Ser Gln Asn  
 305 310 315 320

Gln Gln Glu Lys Asn Glu Gln Glu Leu Leu Ser Arg Pro Gly Gly Thr  
 325 330 335

Met Ala Phe Ser Pro Glu Val Ile Pro Met Phe Ser Ala Leu Ser Glu  
 340 345 350

Gly Ala Thr Pro Gln Asp Leu Pro Ile Val Gln Asn Ile Gln Gly Gln  
 355 360 365

Met Val His Gln Ala Ile Ser Pro Arg Thr Leu Asn Ala Gly Pro Gly  
 370 375 380

Pro Leu Gln Glu Gln Ile Gly Trp Met Thr Asn Asn Pro Pro Ile Pro  
 385 390 395 400

Val Gly Glu Ile Tyr Lys Arg Trp Ile Ile Leu Gly Leu Asn Lys Ile  
 405 410 415

Val Arg Met Tyr Ser Pro Thr Ser Ile Leu Asp Ile Arg Gln Gly Pro  
 420 425 430

Lys Glu Pro Phe Arg Asp Tyr Val Asp Arg Phe Tyr Lys Glu Ile Cys  
 435 440 445

Thr Glu Met Glu Lys Glu Gly Lys Ile Ser Lys Ile Gly Pro Gly Pro  
 450 455 460

Gly Pro Phe Arg Lys Tyr Thr Ala Phe Thr Ile Pro Ser Ile Asn Asn  
 465 470 475 480

Glu Ser Pro Ala Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Glu Pro  
 485 490 495

Trp Glu Phe Val Asn Thr Pro Pro Leu Val Lys Leu Trp Tyr Gln Lys  
 500 505 510

Thr Ala Val Gln Met Ala Val Phe Ile His Asn Phe Lys Arg Gln Lys  
515 520 525

Gln Ile Thr Lys Ile Gln Asn Phe Arg Val Tyr Tyr Arg Gly Pro Gly  
530 535 540

Pro Gln Leu Leu Phe Ile His Phe Arg Ser Arg Gln Arg Arg Arg Arg  
545 550 555 560

Tyr Ser Ser Leu Ile Arg Arg Thr Val Arg Ile Ser Ser Ser Ser Arg  
565 570 575

Leu Trp Arg Gln Pro Met Arg Lys Trp Met Asn Ser Ser Ile Ser Gly  
580 585 590

Pro Gly Pro Asp Met Arg Asp Asn Trp Arg Ser Glu Leu Tyr Lys Tyr  
595 600 605

Lys Val Gln Gln His Leu Leu Gln Leu Thr Val Trp Gly Ile Lys Gln  
610 615 620

Leu Ala Ser Leu Trp Asn Trp Phe Asp Ile Thr Asn Trp Leu Trp Tyr  
625 630 635 640

Ile Lys Ile Phe Ile Met Ile Val Gly Gly Leu Ile Gly Leu Arg His  
645 650 655

Ile Pro Arg Arg Ile Arg Gln Gly Leu Glu Arg Ala Leu Arg Ala Ala  
660 665 670

Trp Thr Arg Ala Pro Pro Thr Ser Ala Pro Pro Arg Gly Gln Gly Ser  
675 680 685

Met Asp Glu Gly Thr Ala Asp Glu Arg Ala Pro Leu Ile Arg Thr  
690 695 700

<210> 9  
<211> 2063  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Construct encoding polyepitope polypeptide.

<220>  
 <221> CDS  
 <222> (7)..(2061)  
 <223> Sequence encoding MCMVABTh polyepitope polypeptide.

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tgc cag gtg tgc ttc acc acc ggc ccc ggc ccc cgc cag cgc cgc cgc	96
Cys Gln Val Cys Phe Thr Thr Gly Pro Gly Pro Arg Gln Arg Arg Arg	
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gcc ccc cag gac agc cag acc cac cag gtg agc gta tac tac gcc gcc	144
Ala Pro Gln Asp Ser Gln Thr His Gln Val Ser Val Tyr Tyr Ala Ala	
35 40 45	
gcc cag tgg gac ttc ggc aac acc atg tgc cag atc aat ccc ggc cgc	192
Ala Gln Trp Asp Phe Gly Asn Thr Met Cys Gln Ile Asn Pro Gly Arg	
50 55 60	
agc cag aag gag ggc ctg cac tac acc tgc gta tac ggc ccc ggc ccc	240
Ser Gln Lys Glu Gly Leu His Tyr Thr Cys Val Tyr Gly Pro Gly Pro	
65 70 75	
ccc tgc aac aag tgc tac tgc aag aag tgc tgc tac cac tgc cag gtg	288
Pro Cys Asn Lys Cys Tyr Cys Lys Lys Cys Cys Tyr His Cys Gln Val	
80 85 90	
tgc ttc ctg aac aat ccc ggc aag cag cgc cgc ggc acc ccc cag agc	336
Cys Phe Leu Asn Asn Pro Gly Lys Gln Arg Arg Gly Thr Pro Gln Ser	
95 100 105 110	
aac aag gac cac cag aac ccc ggc cct gga ccc aac gag cag gac ctg	384
Asn Lys Asp His Gln Asn Pro Gly Pro Gly Pro Asn Glu Gln Asp Leu	
115 120 125	
ctg gcc ctg gac aag tgg gcc aac ctg tgg aac tgg ttc gac atc agc	432
Leu Ala Leu Asp Lys Trp Ala Asn Leu Trp Asn Trp Phe Asp Ile Ser	
130 135 140	
aat ccc ggc gcc tgc aac acc tgc tac tgc aag aag tgc agc tac cac	480
Asn Pro Gly Ala Cys Asn Thr Cys Tyr Cys Lys Lys Cys Ser Tyr His	
145 150 155	
tgc ctg gtg tgc ttc cag acc ggc ccc ggc ccc cgc cag cgc cgc agc	528
Cys Leu Val Cys Phe Gln Thr Gly Pro Gly Pro Arg Gln Arg Arg Ser	
160 165 170	
gcc ccc ccc agc agc gag gac cac cag aac ctg aat ccc ggc aac gag	576
Ala Pro Pro Ser Ser Glu Asp His Gln Asn Leu Asn Pro Gly Asn Glu	
175 180 185 190	
cag gag ctg ctg gag ctg gac aag tgg gcc agc ctg tgg aac tgg ttc	624
Gln Glu Leu Leu Glu Leu Asp Lys Trp Ala Ser Leu Trp Asn Trp Phe	

195										200					205					
gac atc acc ggc cca gga ccc cac gag cgc agc tac atg ttc agc gac	672																			
Asp Ile Thr Gly Pro Gly Pro His Glu Arg Ser Tyr Met Phe Ser Asp																				
210 215 220																				
ctg gag aac cgc tgc atc aac gag aag gac ctg ctg gcc ctg gac aag	720																			
Leu Glu Asn Arg Cys Ile Asn Glu Lys Asp Leu Leu Ala Leu Asp Lys																				
225 230 235																				
tgg cag aac ctg tgg agc tgg ttc gac atc acc aac cct ggc agc ggc	768																			
Trp Gln Asn Leu Trp Ser Trp Phe Asp Ile Thr Asn Pro Gly Ser Gly																				
240 245 250																				
atc gtg cag cag cag aac aac ctg ctg cgc gcc atc gag gcc cag cag	816																			
Ile Val Gln Gln Gln Asn Asn Leu Leu Arg Ala Ile Glu Ala Gln Gln																				
255 260 265 270																				
cac ctg ctg cag ctg acc acc gtg tgg ggc atc aag cag ctg cag gcc	864																			
His Leu Leu Gln Leu Thr Thr Val Trp Gly Ile Lys Gln Leu Gln Ala																				
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cgc atc ctg aat ccc ggc ggt cct gga cca tgg atg gag tgg gac cgc	912																			
Arg Ile Leu Asn Pro Gly Gly Pro Gly Pro Trp Met Glu Trp Asp Arg																				
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gag atc aac aac tac acc agc ctg atc cac agc ctg atc gag gag agc	960																			
Glu Ile Asn Asn Tyr Thr Ser Leu Ile His Ser Leu Ile Glu Glu Ser																				
305 310 315																				
cag aac cag cag gag aag aac gag cag gag ctg ctg tct aga ccc ggc	1008																			
Gln Asn Gln Gln Glu Lys Asn Glu Gln Glu Leu Leu Ser Arg Pro Gly																				
320 325 330																				
ggt acc atg gcc ttc agc ccc gag gtg atc ccc atg ttc agc gcc ctg	1056																			
Gly Thr Met Ala Phe Ser Pro Glu Val Ile Pro Met Phe Ser Ala Leu																				
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agc gag ggc gcc acc ccc cag gac ctg ccc atc gtg cag aac atc cag	1104																			
Ser Glu Gly Ala Thr Pro Gln Asp Leu Pro Ile Val Gln Asn Ile Gln																				
355 360 365																				
ggc cag atg gtg cac cag gcc atc agc ccc cgc acc ctg aac gcc ggc	1152																			
Gly Gln Met Val His Gln Ala Ile Ser Pro Arg Thr Leu Asn Ala Gly																				
370 375 380																				
ccc ggc ccc ctg cag gag cag atc ggc tgg atg acc aac aac ccc ccc	1200																			
Pro Gly Pro Leu Gln Glu Gln Ile Gly Trp Met Thr Asn Asn Pro Pro																				
385 390 395																				
atc ccc gtg ggc gag atc tac aag cgc tgg atc atc ctg ggc ctg aac	1248																			
Ile Pro Val Gly Glu Ile Tyr Lys Arg Trp Ile Ile Leu Gly Leu Asn																				
400 405 410																				
aag atc gtg cgc atg tac agc ccc acc agc atc ctg gac atc cgc cag	1296																			
Lys Ile Val Arg Met Tyr Ser Pro Thr Ser Ile Leu Asp Ile Arg Gln																				
415 420 425 430																				

ggc ccc aag gag ccc ttc cgc gac tac gtg gac cgc ttc tac aag gag Gly Pro Lys Glu Pro Phe Arg Asp Tyr Val Asp Arg Phe Tyr Lys Glu 435 440 445	1344
atc tgc acc gag atg gag aag gag ggc aag atc agc aag atc ggc ccc Ile Cys Thr Glu Met Glu Lys Glu Gly Lys Ile Ser Lys Ile Gly Pro 450 455 460	1392
ggc ccc ggc ccc ttc cgc aag tac acc gcc ttc acc atc ccc agc atc Gly Pro Gly Pro Phe Arg Lys Tyr Thr Ala Phe Thr Ile Pro Ser Ile 465 470 475	1440
aac aac gag agc ccc gcc atc ttc cag agc agc atg acc aag atc ctg Asn Asn Glu Ser Pro Ala Ile Phe Gln Ser Ser Met Thr Lys Ile Leu 480 485 490	1488
gag ccc tgg gag ttc gtg aac acc ccc ccc ctg gtg aag ctg tgg tac Glu Pro Trp Glu Phe Val Asn Thr Pro Pro Leu Val Lys Leu Trp Tyr 495 500 505 510	1536
cag aag acc gcc gtg cag atg gcc gtg ttc atc cac aac ttc aag cgc Gln Lys Thr Ala Val Gln Met Ala Val Phe Ile His Asn Phe Lys Arg 515 520 525	1584
cag aag cag atc acc aag atc cag aac ttc cgc gtg tac tac cgc ggc Gln Lys Gln Ile Thr Lys Ile Gln Asn Phe Arg Val Tyr Tyr Arg Gly 530 535 540	1632
ccc ggc ccc cag ctg ctg ttc atc cac ttc cgc tcg cgc cag cgg cgg Pro Gly Pro Gln Leu Leu Phe Ile His Phe Arg Ser Arg Gln Arg Arg 545 550 555	1680
cgg cgg tac agc agc ttg atc agg cgc acg gtg cgg atc agc tcc tcg Arg Arg Tyr Ser Ser Leu Ile Arg Arg Thr Val Arg Ile Ser Ser Ser 560 565 570	1728
tcg cgg ctg tgg cgg cag ccg atg cgg aag tgg atg aac agc agc atc Ser Arg Leu Trp Arg Gln Pro Met Arg Lys Trp Met Asn Ser Ser Ile 575 580 585 590	1776
agc ggc ccc ggc ccc gac atg cgc gac aac tgg cgc agc gag ctg tac Ser Gly Pro Gly Pro Asp Met Arg Asp Asn Trp Arg Ser Glu Leu Tyr 595 600 605	1824
aag tac aag gtg cag cag cac ctg ctg cag ctg acc gtg tgg ggc atc Lys Tyr Lys Val Gln Gln His Leu Leu Gln Leu Thr Val Trp Gly Ile 610 615 620	1872
aag cag ctg gcc agc ctg tgg aac tgg ttc gac atc acc aac tgg ctg Lys Gln Leu Ala Ser Leu Trp Asn Trp Phe Asp Ile Thr Asn Trp Leu 625 630 635	1920
tgg tac atc aag atc ttc atc atg atc gtg ggc ggc ctg atc ggc ctg Trp Tyr Ile Lys Ile Phe Ile Met Ile Val Gly Gly Leu Ile Gly Leu 640 645 650	1968

cgc cac atc ccc cgc cgc atc cgc cag ggc ctg gag cgc gcc ctg agg 2016  
 Arg His Ile Pro Arg Arg Ile Arg Gln Gly Leu Glu Arg Ala Leu Arg  
 655 660 665 670

gca gca tgg acg agg gca ccg ccg acg agc gcg ccc ccc gtt taa ac 2063  
 Ala Ala Trp Thr Arg Ala Pro Pro Thr Ser Ala Pro Pro Val  
 675 680

<210> 10  
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<220>  
 <223> Construct encoding polyepitope polypeptide.

<400> 10

Met Ala Cys Thr Asn Cys Tyr Cys Lys Lys Cys Cys Phe His Cys Gln  
 1 5 10 15

Val Cys Phe Thr Thr Gly Pro Gly Pro Arg Gln Arg Arg Arg Ala Pro  
 20 25 30

Gln Asp Ser Gln Thr His Gln Val Ser Val Tyr Tyr Ala Ala Ala Gln  
 35 40 45

Trp Asp Phe Gly Asn Thr Met Cys Gln Ile Asn Pro Gly Arg Ser Gln  
 50 55 60

Lys Glu Gly Leu His Tyr Thr Cys Val Tyr Gly Pro Gly Pro Pro Cys  
 65 70 75 80

Asn Lys Cys Tyr Cys Lys Lys Cys Cys Tyr His Cys Gln Val Cys Phe  
 85 90 95

Leu Asn Asn Pro Gly Lys Gln Arg Arg Gly Thr Pro Gln Ser Asn Lys  
 100 105 110

Asp His Gln Asn Pro Gly Pro Gly Pro Asn Glu Gln Asp Leu Leu Ala  
 115 120 125

Leu Asp Lys Trp Ala Asn Leu Trp Asn Trp Phe Asp Ile Ser Asn Pro  
 130 135 140

Gly Ala Cys Asn Thr Cys Tyr Cys Lys Lys Cys Ser Tyr His Cys Leu  
 145 150 155 160

Val Cys Phe Gln Thr Gly Pro Gly Pro Arg Gln Arg Arg Ser Ala Pro  
165 170 175

Pro Ser Ser Glu Asp His Gln Asn Leu Asn Pro Gly Asn Glu Gln Glu  
180 185 190

Leu Leu Glu Leu Asp Lys Trp Ala Ser Leu Trp Asn Trp Phe Asp Ile  
195 200 205

Thr Gly Pro Gly Pro His Glu Arg Ser Tyr Met Phe Ser Asp Leu Glu  
210 215 220

Asn Arg Cys Ile Asn Glu Lys Asp Leu Leu Ala Leu Asp Lys Trp Gln  
225 230 235 240

Asn Leu Trp Ser Trp Phe Asp Ile Thr Asn Pro Gly Ser Gly Ile Val  
245 250 255

Gln Gln Gln Asn Asn Leu Leu Arg Ala Ile Glu Ala Gln Gln His Leu  
260 265 270

Leu Gln Leu Thr Thr Val Trp Gly Ile Lys Gln Leu Gln Ala Arg Ile  
275 280 285

Leu Asn Pro Gly Gly Pro Gly Pro Trp Met Glu Trp Asp Arg Glu Ile  
290 295 300

Asn Asn Tyr Thr Ser Leu Ile His Ser Leu Ile Glu Glu Ser Gln Asn  
305 310 315 320

Gln Gln Glu Lys Asn Glu Gln Glu Leu Leu Ser Arg Pro Gly Gly Thr  
325 330 335

Met Ala Phe Ser Pro Glu Val Ile Pro Met Phe Ser Ala Leu Ser Glu  
340 345 350

Gly Ala Thr Pro Gln Asp Leu Pro Ile Val Gln Asn Ile Gln Gly Gln  
355 360 365

Met Val His Gln Ala Ile Ser Pro Arg Thr Leu Asn Ala Gly Pro Gly  
370 375 380

Pro Leu Gln Glu Gln Ile Gly Trp Met Thr Asn Asn Pro Pro Ile Pro  
 385 390 395 400

Val Gly Glu Ile Tyr Lys Arg Trp Ile Ile Leu Gly Leu Asn Lys Ile  
 405 410 415

Val Arg Met Tyr Ser Pro Thr Ser Ile Leu Asp Ile Arg Gln Gly Pro  
 420 425 430

Lys Glu Pro Phe Arg Asp Tyr Val Asp Arg Phe Tyr Lys Glu Ile Cys  
 435 440 445

Thr Glu Met Glu Lys Glu Gly Lys Ile Ser Lys Ile Gly Pro Gly Pro  
 450 455 460

Gly Pro Phe Arg Lys Tyr Thr Ala Phe Thr Ile Pro Ser Ile Asn Asn  
 465 470 475 480

Glu Ser Pro Ala Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Glu Pro  
 485 490 495

Trp Glu Phe Val Asn Thr Pro Pro Leu Val Lys Leu Trp Tyr Gln Lys  
 500 505 510

Thr Ala Val Gln Met Ala Val Phe Ile His Asn Phe Lys Arg Gln Lys  
 515 520 525

Gln Ile Thr Lys Ile Gln Asn Phe Arg Val Tyr Tyr Arg Gly Pro Gly  
 530 535 540

Pro Gln Leu Leu Phe Ile His Phe Arg Ser Arg Gln Arg Arg Arg Arg  
 545 550 555 560

Tyr Ser Ser Leu Ile Arg Arg Thr Val Arg Ile Ser Ser Ser Ser Arg  
 565 570 575

Leu Trp Arg Gln Pro Met Arg Lys Trp Met Asn Ser Ser Ile Ser Gly  
 580 585 590

Pro Gly Pro Asp Met Arg Asp Asn Trp Arg Ser Glu Leu Tyr Lys Tyr  
 595 600 605

Lys Val Gln Gln His Leu Leu Gln Leu Thr Val Trp Gly Ile Lys Gln  
610 615 620

Leu Ala Ser Leu Trp Asn Trp Phe Asp Ile Thr Asn Trp Leu Trp Tyr  
625 630 635 640

Ile Lys Ile Phe Ile Met Ile Val Gly Gly Leu Ile Gly Leu Arg His  
645 650 655

Ile Pro Arg Arg Ile Arg Gln Gly Leu Glu Arg Ala Leu Arg Ala Ala  
660 665 670

Trp Thr Arg Ala Pro Pro Thr Ser Ala Pro Pro Val  
675 680

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<211> 14  
<212> PRT  
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<220>  
<223> HIV-1 antigenic fragment/epitope.

<400> 11

Trp Lys Gly Ser Pro Ala Ile Phe Gln Ser Ser Met Thr Lys  
1 5 10

<210> 12  
<211> 13  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> HIV-1 antigenic fragment/epitope.

<400> 12

Ala Val Arg His Phe Pro Arg Ile Trp Leu His Ser Leu  
1 5 10

<210> 13  
<211> 13  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> HIV-1 antigenic fragment/epitope.

<400> 13

Ala Val Arg His Phe Pro Arg Pro Trp Leu His Gly Leu  
 1 5 10

<210> 14  
 <211> 9  
 <212> PRT  
 <213> Artificial Sequence

<220>  
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<400> 14

Glu Arg Tyr Leu Lys Asp Gln Gln Leu  
 1 5

<210> 15  
 <211> 16  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> HIV-1 antigenic fragment/epitope.

<400> 15

Ile Pro Met Phe Ser Ala Leu Ser Glu Gly Ala Thr Pro Asp Gln Leu  
 1 5 10 15

<210> 16  
 <211> 15  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> HIV-1 antigenic fragment/epitope.

<400> 16

Asn Pro Pro Ile Pro Val Gly Glu Ile Tyr Lys Arg Trp Ile Ile  
 1 5 10 15

<210> 17  
 <211> 13  
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<220>  
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<400> 17

Trp Lys Gly Ser Pro Ala Ile Phe Gln Ser Ser Met Thr  
1 5 10

<210> 18  
<211> 9  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> HIV-1 antigenic fragment/epitope.

<400> 18

Ala Ile Phe Gln Ser Ser Met Thr Lys  
1 5

<210> 19  
<211> 15  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> HIV-1 antigenic fragment/epitope.

<400> 19

Val Gly Phe Pro Val Thr Pro Gln Val Pro Leu Arg Pro Met Thr  
1 5 10 15

<210> 20  
<211> 11  
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<213> Artificial Sequence

<220>  
<223> HIV-1 antigenic fragment/epitope.

<400> 20

Arg Ile Arg Thr Thr Trp Lys Ser Leu Val Lys  
1 5 10

<210> 21  
<211> 13  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> HIV-1 antigenic fragment/epitope.

<400> 21

Ala Val Arg His Phe Pro Arg Ile Trp Leu His Ser Leu

1 5 10

<210> 22  
<211> 13  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> HIV-1 antigenic fragment/epitope.

<400> 22

Ala Val Arg His Phe Pro Arg Pro Trp Leu His Gly Leu  
1 5 10

<210> 23  
<211> 9  
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<213> Artificial Sequence

<220>  
<223> Control peptide.

<400> 23

Val Ser Asp Gly Gly Pro Asn Leu Tyr  
1 5

<210> 24  
<211> 9  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Control peptide.

<400> 24

Cys Thr Glu Leu Lys Leu Ser Asp Tyr  
1 5

<210> 25  
<211> 9  
<212> PRT  
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<220>  
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<400> 25

Gly Leu Cys Thr Leu Val Ala Met Leu  
1 5

<210> 26  
<211> 9  
<212> PRT  
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<220>  
<223> Control peptide.

<400> 26

Gly Ile Leu Gly Phe Val Phe Thr Leu  
1 5

<210> 27  
<211> 9  
<212> PRT  
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<220>  
<223> Control peptide.

<400> 27

Asn Leu Val Pro Met Val Ala Thr Val  
1 5

<210> 28  
<211> 9  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Control peptide.

<400> 28

Ile Leu Arg Gly Ser Val Ala His Lys  
1 5

<210> 29  
<211> 9  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Control peptide.

<400> 29

Arg Val Arg Ala Tyr Thr Tyr Ser Lys  
1 5

<210> 30  
<211> 9  
<212> PRT  
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<220>  
<223> Control peptide.

<400> 30

Arg Leu Arg Ala Glu Ala Gln Val Lys  
1 5

<210> 31  
<211> 9  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Control peptide.

<400> 31

Ile Val Thr Asp Phe Ser Val Ile Lys  
1 5

<210> 32  
<211> 9  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Control peptide.

<400> 32

Ala Thr Ile Gly Thr Ala Met Tyr Lys  
1 5

<210> 33  
<211> 10  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Control peptide.

<400> 33

Asp Tyr Cys Asn Val Leu Asn Lys Glu Phe  
1 5 10

<210> 34  
<211> 9  
<212> PRT  
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<220>  
<223> Control peptide.

<400> 34

Lys Thr Gly Gly Pro Ile Tyr Lys Arg  
1 5

<210> 35  
<211> 9  
<212> PRT  
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<220>  
<223> Control peptide.

<400> 35

Arg Pro Pro Ile Phe Ile Arg Arg Leu  
1 5

<210> 36  
<211> 10  
<212> PRT  
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<220>  
<223> Control peptide.

<400> 36

Thr Pro Arg Val Thr Gly Gly Gly Ala Met  
1 5 10

<210> 37  
<211> 9  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Control peptide.

<400> 37

Gln Ala Lys Trp Arg Leu Gln Thr Leu  
1 5

<210> 38

<211> 9  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Control peptide.

<400> 38

Phe Leu Arg Gly Arg Ala Tyr Gly Leu  
1 5

<210> 39  
<211> 8  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Control peptide.

<400> 39

Arg Ala Lys Phe Lys Gln Leu Leu  
1 5

<210> 40  
<211> 9  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Control peptide.

<400> 40

Glu Leu Arg Ser Arg Tyr Trp Ala Ile  
1 5

<210> 41  
<211> 9  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Control peptide.

<400> 41

Ser Arg Tyr Trp Ala Ile Arg Thr Arg  
1 5

<210> 42  
<211> 9

<212> PRT  
<213> Artificial Sequence

<220>  
<223> Control peptide.

<400> 42

Arg Arg Ile Tyr Asp Leu Ile Glu Leu  
1 5

<210> 43  
<211> 9  
<212> PRT  
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<220>  
<223> Control peptide.

<400> 43

Tyr Pro Leu His Glu Gln His Gly Met  
1 5

<210> 44  
<211> 10  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Control peptide.

<400> 44

Glu Glu Asn Leu Leu Asp Phe Val Arg Phe  
1 5 10

<210> 45  
<211> 15  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Control peptide.

<400> 45

Gln Glu Phe Phe Trp Asp Ala Asn Asp Ile Tyr Arg Ile Phe Ala  
1 5 10 15

<210> 46  
<211> 20  
<212> PRT

<213> Artificial Sequence

<220>

<223> HIV-1 antigenic fragment/epitope.

<400> 46

Pro Cys Asn Lys Cys Tyr Cys Lys Lys Cys Cys Tyr His Cys Gln Val  
1 5 10 15

Cys Phe Ile Thr  
20

<210> 47

<211> 20

<212> PRT

<213> Artificial Sequence

<220>

<223> HIV-1 antigenic fragment/epitope.

<400> 47

Ala Cys Ser Lys Cys Tyr Cys Lys Lys Cys Cys Trp His Cys Gln Leu  
1 5 10 15

Cys Phe Leu Lys  
20

<210> 48

<211> 20

<212> PRT

<213> Artificial Sequence

<220>

<223> HIV-1 antigenic fragment/epitope.

<400> 48

Pro Cys Thr Lys Cys Tyr Cys Lys Arg Cys Cys Phe His Cys Gln Trp  
1 5 10 15

Cys Phe Ile Thr  
20

<210> 49

<211> 20

<212> PRT

<213> Artificial Sequence

<220>

<223> HIV-1 antigenic fragment/epitope.

<400> 49

Ala Cys Ser Lys Cys Tyr Cys His Ile Cys Cys Trp His Cys Gln Leu  
1 5 10 15

Cys Phe Leu Asn  
20

<210> 50

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> HIV-1 antigenic fragment/epitope.

<400> 50

Arg Gln Arg Arg Arg Pro Pro Gln Gly Gly Gln Ala His Gln Asp Pro  
1 5 10 15

<210> 51

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> HIV-1 antigenic fragment/epitope.

<400> 51

Lys His Arg Arg Gly Thr Pro Gln Ser Ser Lys Asp His Gln Asn Pro  
1 5 10 15

<210> 52

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> HIV-1 antigenic fragment/epitope.

<400> 52

Arg Arg Arg Arg Gly Thr Pro Gln Ser Arg Gln Asp His Gln Asn Pro  
1 5 10 15

<210> 53

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> HIV-1 antigenic fragment/epitope.

<400> 53

Arg	Gln	Arg	His	Arg	Thr	Pro	Gln	Ser	Ser	Gln	Ile	His	Gln	Asp	Pro
1				5					10					15	

<210> 54

<211> 21

<212> PRT

<213> Artificial Sequence

<220>

<223> HIV-1 antigenic fragment/epitope.

<400> 54

Asn	Glu	Lys	Glu	Leu	Leu	Glu	Leu	Asp	Lys	Trp	Ala	Ser	Leu	Trp	Asn
1				5					10					15	

Trp	Phe	Ser	Ile	Thr
			20	

<210> 55

<211> 21

<212> PRT

<213> Artificial Sequence

<220>

<223> HIV-1 antigenic fragment/epitope.

<400> 55

Asn	Glu	Gln	Glu	Leu	Leu	Ala	Leu	Asp	Lys	Trp	Ala	Ser	Leu	Trp	Asn
1				5					10					15	

Trp	Phe	Asp	Ile	Ser
			20	

<210> 56

<211> 21

<212> PRT

<213> Artificial Sequence

<220>

<223> HIV-1 antigenic fragment/epitope.

<400> 56

Asn Glu Gln Asp Leu Leu Ala Leu Asp Lys Trp Ala Ser Leu Trp Thr  
 1 5 10 15

Trp Phe Ser Ile Thr  
 20

<210> 57  
 <211> 36  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> HIV-1 antigenic fragment/epitope.

<400> 57

Ser Gly Ile Val Gln Gln Asn Asn Leu Leu Arg Ala Ile Glu Ala  
 1 5 10 15

Gln Gln His Leu Leu Gln Leu Thr Val Trp Gly Ile Lys Gln Leu Gln  
 20 25 30

Ala Arg Ile Leu  
 35

<210> 58  
 <211> 15  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> HIV-1 antigenic fragment/epitope.

<400> 58

Tyr Ala Ala Ala Gln Trp Asp Phe Gly Asn Thr Met Cys Gln Leu  
 1 5 10 15

<210> 59  
 <211> 20  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> HIV-1 antigenic fragment/epitope.

<400> 59

Cys Ser Ser His Phe Pro Tyr Ser Gln Tyr Gln Phe Trp Lys Asn Phe  
 1 5 10 15

Gln Thr Leu Lys  
20

<210> 60  
<211> 15  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> HIV-1 antigenic fragment/epitope.

<400> 60

Ser Pro Val Ser Ile Leu Asp Ile Arg Gln Gly Pro Lys Glu Pro  
1 5 10 15

<210> 61  
<211> 15  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> HIV-1 antigenic fragment/epitope.

<400> 61

Gln Leu Leu Phe Ile His Phe Arg Ile Gly Cys Arg His Ser Arg  
1 5 10 15

<210> 62  
<211> 15  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> HIV-1 antigenic fragment/epitope.

<400> 62

Asp Glu Glu Leu Ile Arg Thr Val Arg Leu Ile Lys Leu Leu Tyr  
1 5 10 15

<210> 63  
<211> 16  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> HIV-1 antigenic fragment/epitope.

<400> 63

Arg	Arg	Arg	Arg	Trp	Arg	Glu	Arg	Gln	Arg	Gln	Ile	His	Ser	Ile	Ser
1				5				10						15	

<210> 64

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> HIV-1 antigenic fragment/epitope.

<400> 64

His	Ile	Pro	Arg	Arg	Ile	Arg	Gln	Gly	Leu	Glu	Arg	Ala	Leu	Leu
1				5				10					15	